

FIG. 1

Schematic diagram showing domain organization of scFv (UCHT-1)-PE38 molecule (SEQ. ID. No. 1), prepared in Example 1, consisting of an N-terminal light chain variable region (V_L) of 109 residues, a peptide linker (L) of 16 residues, a heavy chain variable region (V_H) of 122 amino acids, a connector segment (C) of 5 amino acids (KASGG) (SEQ. ID. No. 9), and the PE38 mutant, comprising 347 amino acids ("Toxin").

On page 12, please replace the description of Figure 15 with the following replacement description:

FIG. 15

Nucleotide (SEQ. ID. No. 2), and amino acid sequence (SEQ. ID. No. 1), of scFv (UCHT-1)-PE38. DNA sequence encoding the NcoI, HindIII, EcoRI, and BamHI/BglII restriction sites used for subcloning, are underlined; the flexible linker separating the V_L from the V_H domains is also underlined. Numbers correspond to nucleotides. Single letter codes denote encoded amino acids. The amino-terminal residues Met and Ala are encoded by the NcoI restriction site that was added to facilitate expression from the *E. coli* plasmid pET 15b. The 3' non-coding DNA between the EcoRI site and the BglII/BamHI site is carry-over sequence from the polylinker of an intermediate cloning vector (pLitmus 38, New England Biolabs).